

SEQUENCE LISTING

<110> MOECKEL, Bettina
BATHE, Brigitte
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<120> Nucleotide sequences coding for the rpoB gene

<130> 219774US0XCIP

<140> new application
<141> 2002-02-19

<150> DE 10107229.5
<151> 2001-02-16

<150> US 09/887052
<151> 2001-06-25

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<170> PatentIn version 3.1

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<400> 3
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aaaatattga tgattttac ggcgaccgca gcggccagaa gtacgaacag aaattgcttt 120
tcgacgcctc cctcgacgat gcagctgtct ctaagctggt tgcacagggcc gaaagcatcc 180
ctgatggaga tgtgagcaaa atcgcaaata ccgtaggtat tgtgatcggt gcggatttgg 240
ctctcggtgg cctggccggg tgggggggg cggtggaa gaaacgtcga gaagcttaac 300
ctgctgttca aatagatttt ccctgtttcg aattgcggaa accccgggtt tggttgcgt 360
gggcctcgta agaaggggtc aagaagattt ctgggaaacg cggccgtgcg gttgggttgc 420
aatagcacgc ggagcaccag atgaaaaatc tccccttac tttcgccgc gattggata 480
ctctgagtcg ttgcgttggaa attcgtgact cttttcggtt cctgtagcgc caagaccc 540

atcaagggtgg tttaaaaaaaaa ccgatttgac aaggtcattc agtgctatct ggagtcggtc	600
agggggatcg ggccctcag cagaccaatt gctcaaaaat accagcggtg ttgatctgca	660
cttaatggcc ttgaccagcc aggtgcaatt acccgcgta g gtg ctg gaa gga ctc Val Leu Glu Gly Leu	716
1 5	
atc ttg gca gtc tcc cgc cag acc aag tca gtc gtc gat att ccc ggt Ile Leu Ala Val Ser Arg Gln Thr Lys Ser Val Val Asp Ile Pro Gly	764
10 15 20	
gca ccg cag cgt tat tct ttc gcg aag gtg tcc gca ccc att gag gtg Ala Pro Gln Arg Tyr Ser Phe Ala Lys Val Ser Ala Pro Ile Glu Val	812
25 30 35	
ccc ggg cta cta gat ctt caa ctg gat tct tac tcc tgg ctg att ggt Pro Gly Leu Leu Asp Leu Gln Leu Asp Ser Tyr Ser Trp Leu Ile Gly	860
40 45 50	
acg cct gag tgg cgt gct cgt cag aag gaa gaa ttc ggc gag gga gcc Thr Pro Glu Trp Arg Ala Arg Gln Lys Glu Glu Phe Gly Glu Gly Ala	908
55 60 65	
cgc gta acc agc ggc ctt gag aac att ctc gag gag ctc tcc cca atc Arg Val Thr Ser Gly Leu Glu Asn Ile Leu Glu Glu Leu Ser Pro Ile	956
70 75 80 85	
cag gat tac tct gga aac atg tcc ctg agc ctt tcg gag cca cgc ttc Gln Asp Tyr Ser Gly Asn Met Ser Leu Ser Leu Ser Glu Pro Arg Phe	1004
90 95 100	
gaa gac gtc aag aac acc att gac gag gcg aaa gaa aag gac atc aac Glu Asp Val Lys Asn Thr Ile Asp Glu Ala Lys Glu Lys Asp Ile Asn	1052
105 110 115	
tac gcg gcg cca ctg tat gtg acc gcg gag ttc gtc aac aac acc acc Tyr Ala Ala Pro Leu Tyr Val Thr Ala Glu Phe Val Asn Asn Thr Thr	1100
120 125 130	
ggt gaa atc aag tct cag act gtc ttc atc ggc gat ttc cca atg atg Gly Glu Ile Lys Ser Gln Thr Val Phe Ile Gly Asp Phe Pro Met Met	1148
135 140 145	
acg gac aag gga acg ttc atc atc aac gga acc gaa cgc gtt gtg gtc Thr Asp Lys Gly Thr Phe Ile Ile Asn Gly Thr Glu Arg Val Val Val	1196
150 155 160 165	
agc cag ctc gtc cgc tcc ccg ggc gtg tac ttt gac cag acc atc gat Ser Gln Leu Val Arg Ser Pro Gly Val Tyr Phe Asp Gln Thr Ile Asp	1244
170 175 180	
aag tca act gag cgt cca ctg cac gcc gtg aag gtt att cct ttc cgt Lys Ser Thr Glu Arg Pro Leu His Ala Val Lys Val Ile Pro Phe Arg	1292
185 190 195	
ggt gct tgg ctt gag ttt gac gtc gat aag cgc gat tcg gtt ggt gtt	1340

Gly Ala Trp Leu Glu Phe Asp Val Asp Lys Arg Asp Ser Val Gly Val			
200	205	210	
cgt att gac cgc aag cgt cgc cag cca gtc acc gta ctg ctg aag gct		1388	
Arg Ile Asp Arg Lys Arg Arg Gln Pro Val Thr Val Leu Leu Lys Ala			
215	220	225	
ctt ggc tgg acc act gag cag atc acc gag cgt ttc ggt ttc tct gaa		1436	
Leu Gly Trp Thr Thr Glu Gln Ile Thr Glu Arg Phe Gly Phe Ser Glu			
230	235	240	245
atc atg atg tcc acc ctc gag tcc gat ggt gta gca aac acc gat gag		1484	
Ile Met Met Ser Thr Leu Glu Ser Asp Gly Val Ala Asn Thr Asp Glu			
250	255	260	
gca ttg ctg gag atc tac cgc aag cag cgt cca ggc gag cag cct acc		1532	
Ala Leu Leu Glu Ile Tyr Arg Lys Gln Arg Pro Gly Glu Gln Pro Thr			
265	270	275	
cgc gac ctt gcg cag tcc ctc ctg gac aac agc ttc ttc cgt gca aag		1580	
Arg Asp Leu Ala Gln Ser Leu Leu Asp Asn Ser Phe Phe Arg Ala Lys			
280	285	290	
cgc tac gac ctg gct cgc gtt ggt cgt tac aag atc aac cgc aag ctc		1628	
Arg Tyr Asp Leu Ala Arg Val Gly Arg Tyr Lys Ile Asn Arg Lys Leu			
295	300	305	
ggc ctt ggt ggc gac cac gat ggt ttg atg act ctt act gaa gag gac		1676	
Gly Leu Gly Gly Asp His Asp Gly Leu Met Thr Leu Thr Glu Glu Asp			
310	315	320	325
atc gca acc acc atc gag tac ctg gtg cgt ctg cac gca ggt gag cgc		1724	
Ile Ala Thr Thr Ile Glu Tyr Leu Val Arg Leu His Ala Gly Glu Arg			
330	335	340	
gtc atg act tct cca aat ggt gaa gag atc cca gtc gag acc gat gac		1772	
Val Met Thr Ser Pro Asn Gly Glu Glu Ile Pro Val Glu Thr Asp Asp			
345	350	355	
atc gac cac ttt ggt aac cgt cgt ctg cgt acc gtt ggc gaa ctg atc		1820	
Ile Asp His Phe Gly Asn Arg Arg Leu Arg Thr Val Gly Glu Leu Ile			
360	365	370	
cag aac cag gtc cgt gtc ggc ctg tcc cgc atg gag cgc gtt gtt cgt		1868	
Gln Asn Gln Val Arg Val Gly Leu Ser Arg Met Glu Arg Val Val Arg			
375	380	385	
gag cgt atg acc acc cag gat gcg gag tcc att act cct act tcc ttg		1916	
Glu Arg Met Thr Thr Gln Asp Ala Glu Ser Ile Thr Pro Thr Ser Leu			
390	395	400	405
atc aac gtt cgt cct gtc tct gca gct atc cgt gag ttc ttc gga act		1964	
Ile Asn Val Arg Pro Val Ser Ala Ala Ile Arg Glu Phe Phe Gly Thr			
410	415	420	
tcc cag ctg tct cag ttc atg gtc cag aac aac tcc ctg tct ggt ttg		2012	
Ser Gln Leu Ser Gln Phe Met Val Gln Asn Asn Ser Leu Ser Gly Leu			

425	430	435	
act cac aag cgt cgt ctg tcg gct ctg ggc ccg ggt ggt ctg tcc cgt Thr His Lys Arg Arg Leu Ser Ala Leu Gly Pro Gly Gly Leu Ser Arg 440	445	450	2060
gag cgc gcc ggc atc gag gtt cga gac gtt cac cca tct cac tac ggc Glu Arg Ala Gly Ile Glu Val Arg Asp Val His Pro Ser His Tyr Gly 455	460	465	2108
cgt atg tgc cca att gag act ccg gaa ggt cca aac att ggc ctg atc Arg Met Cys Pro Ile Glu Thr Pro Glu Gly Pro Asn Ile Gly Leu Ile 470	475	480	2156
ggt tcc ttg gct tcc tat gct cga gtg aac cca ttc ggt ttc att gag Gly Ser Leu Ala Ser Tyr Ala Arg Val Asn Pro Phe Gly Phe Ile Glu 490	495	500	2204
acc cca tac cgt cgc atc atc gac ggc aag ctg acc gac cag att gac Thr Pro Tyr Arg Arg Ile Ile Asp Gly Lys Leu Thr Asp Gln Ile Asp 505	510	515	2252
tac ctt acc gct gat gag gaa gac cgc ttc gtt gtt gcg cag gca aac Tyr Leu Thr Ala Asp Glu Glu Asp Arg Phe Val Val Ala Gln Ala Asn 520	525	530	2300
acg cac tac gac gaa gag ggc aac atc acc gat gag acc gtc act gtt Thr His Tyr Asp Glu Glu Gly Asn Ile Thr Asp Glu Thr Val Thr Val 535	540	545	2348
cgt ctg aag gac ggc gac atc gcc atg gtt ggc cgc aac gcg gtt gat Arg Leu Lys Asp Gly Asp Ile Ala Met Val Gly Arg Asn Ala Val Asp 550	555	560	2396
tac atg gac gtt tcc cct cgt cag atg gtt tct ggt acc gcg atg Tyr Met Asp Val Ser Pro Arg Gln Met Val Ser Val Gly Thr Ala Met 570	575	580	2444
att cca ttc ctg gag cac gac gat gct aac cgt gca ctg atg ggc gcg Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg Ala Leu Met Gly Ala 585	590	595	2492
aac atg cag aag cag gct gtg cca ctg att cgt gcc gag gct cct ttc Asn Met Gln Lys Gln Ala Val Pro Leu Ile Arg Ala Glu Ala Pro Phe 600	605	610	2540
gtg ggc acc ggt atg gag cag cgc gca gca tac gac gcc ggc gac ctg Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr Asp Ala Gly Asp Leu 615	620	625	2588
gtt att acc cca gtc gca ggt gtg gtg gaa aac gtt tca gct gac ttc Val Ile Thr Pro Val Ala Gly Val Val Glu Asn Val Ser Ala Asp Phe 630	635	640	2636
atc acc atc atg gct gat gac ggc aag cgc gaa acc tac ctg ctg cgt Ile Thr Ile Met Ala Asp Asp Gly Lys Arg Glu Thr Tyr Leu Leu Arg 650	655	660	2684

aag ttc cag cgc acc aac cag ggc acc agc tac aac cag aag cct ttg Lys Phe Gln Arg Thr Asn Gln Gly Thr Ser Tyr Asn Gln Lys Pro Leu 665 670 675	2732
gtt aac ttg ggc gag cgc gtt gaa gct ggc cag gtt att gct gat ggt Val Asn Leu Gly Glu Arg Val Glu Ala Gly Gln Val Ile Ala Asp Gly 680 685 690	2780
cca ggt acc ttc aat ggt gaa atg tcc ctt ggc cgt aac ctt ctg gtt Pro Gly Thr Phe Asn Gly Glu Met Ser Leu Gly Arg Asn Leu Leu Val 695 700 705	2828
gcg ttc atg cct tgg gaa ggc cac aac tac gag gat gcg atc atc ctc Ala Phe Met Pro Trp Glu Gly His Asn Tyr Glu Asp Ala Ile Ile Leu 710 715 720 725	2876
aac cag aac atc gtt gag cag gac atc ttg acc tcg atc cac atc gag Asn Gln Asn Ile Val Glu Gln Asp Ile Leu Thr Ser Ile His Ile Glu 730 735 740	2924
gag cac gag atc gat gcc cgc gac act aag ctt ggc gcc gaa gaa atc Glu His Glu Ile Asp Ala Arg Asp Thr Lys Leu Gly Ala Glu Glu Ile 745 750 755	2972
acc cgc gac atc cct aat gtg tct gaa gaa gtc ctc aag gac ctc gac Thr Arg Asp Ile Pro Asn Val Ser Glu Glu Val Leu Lys Asp Leu Asp 760 765 770	3020
gac cgc ggt att gtc cgc atc ggt gct gat gtt cgt gac ggc gac atc Asp Arg Gly Ile Val Arg Ile Gly Ala Asp Val Arg Asp Gly Asp Ile 775 780 785	3068
ctg gtc ggt aag gtc acc cct aag ggc gag acc gag ctc acc ccg gaa Leu Val Gly Lys Val Thr Pro Lys Gly Glu Thr Glu Leu Thr Pro Glu 790 795 800 805	3116
gag cgc ttg ctg cgc gca atc ttc ggt gag aag gcc cgc gaa gtt cgc Glu Arg Leu Leu Arg Ala Ile Phe Gly Glu Lys Ala Arg Glu Val Arg 810 815 820	3164
gat acc tcc atg aag gtg cct cac ggt gag acc ggc aag gtc atc ggc Asp Thr Ser Met Lys Val Pro His Gly Glu Thr Gly Lys Val Ile Gly 825 830 835	3212
gtg cgt cac ttc tcc cgc gag gac gac gat ctg gct cct ggc gtc Val Arg His Phe Ser Arg Glu Asp Asp Asp Asp Leu Ala Pro Gly Val 840 845 850	3260
aac gag atg atc cgt atc tac gtt gct cag aag cgt aag atc cag gac Asn Glu Met Ile Arg Ile Tyr Val Ala Gln Lys Arg Lys Ile Gln Asp 855 860 865	3308
ggc gat aag ctc gct ggc cgc cac ggt aac aag ggt gtt gtc ggt aaa Gly Asp Lys Leu Ala Gly Arg His Gly Asn Lys Gly Val Val Gly Lys 870 875 880 885	3356

att ttg cct cag gaa gat atg cca ttc ctt cca gac ggc act cct gtt Ile Leu Pro Gln Glu Asp Met Pro Phe Leu Pro Asp Gly Thr Pro Val 890 895 900	3404
gac atc atc ttg aac acc cac ggt gtt cca cgt cgt atg aac att ggt Asp Ile Ile Leu Asn Thr His Gly Val Pro Arg Arg Met Asn Ile Gly 905 910 915	3452
cag gtt ctt gag acc cac ctt ggc tgg ctg gca tct gct ggt tgg tcc Gln Val Leu Glu Thr His Leu Gly Trp Leu Ala Ser Ala Gly Trp Ser 920 925 930	3500
gtg gat cct gaa gat cct gag aac gct gag ctc gtc aag act ctg cct Val Asp Pro Glu Asp Pro Glu Asn Ala Glu Leu Val Lys Thr Leu Pro 935 940 945	3548
gca gac ctc ctc gag gtt cct gct ggt tcc ttg act gca act cct gtg Ala Asp Leu Leu Glu Val Pro Ala Gly Ser Leu Thr Ala Thr Pro Val 950 955 960 965	3596
ttc gac ggt gcg tca aac gaa gag ctc gca ggc ctg ctc gct aat tca Phe Asp Gly Ala Ser Asn Glu Glu Leu Ala Gly Leu Leu Ala Asn Ser 970 975 980	3644
cgt cca aac cgc gac ggc gac gtc atg gtt aac gcg gat ggt aaa gca Arg Pro Asn Arg Asp Gly Asp Val Met Val Asn Ala Asp Gly Lys Ala 985 990 995	3692
acg ctt atc gac ggt cgc tcc ggt gag cct tac ccg tac ccg gtt Thr Leu Ile Asp Gly Arg Ser Gly Glu Pro Tyr Pro Tyr Pro Val 1000 1005 1010	3737
tcc atc ggc tac atg tac atg ctg aag ctg cac cac ctc gtt gac Ser Ile Gly Tyr Met Tyr Met Leu Lys Leu His His Leu Val Asp 1015 1020 1025	3782
gag aag atc cac gca cgt tcc act ggt cct tac tcc atg att acc Glu Lys Ile His Ala Arg Ser Thr Gly Pro Tyr Ser Met Ile Thr 1030 1035 1040	3827
cag cag cca ctg ggt ggt aaa gca cag ttc ggt gga cag cgt ttc Gln Gln Pro Leu Gly Gly Lys Ala Gln Phe Gly Gly Gln Arg Phe 1045 1050 1055	3872
ggc gaa atg gag gtg tgg gca atg cag gca tac ggc gct gcc tac Gly Glu Met Glu Val Trp Ala Met Gln Ala Tyr Gly Ala Ala Tyr 1060 1065 1070	3917
aca ctt cag gag ctg ctg acc atc aag tct gat gac gtg gtt ggc Thr Leu Gln Glu Leu Leu Thr Ile Lys Ser Asp Asp Val Val Gly 1075 1080 1085	3962
cgt gtc aag gtc tac gaa gca att gtg aag ggc gag aac atc ccg Arg Val Lys Val Tyr Glu Ala Ile Val Lys Gly Glu Asn Ile Pro 1090 1095 1100	4007
gat cca ggt att cct gag tcc ttc aag gtt ctc ctc aag gag ctc	4052

Asp	Pro	Gly	Ile	Pro	Glu	Ser	Phe	Lys	Val	Leu	Leu	Lys	Glu	Leu	
1105							1110					1115			
cag	tcc	ttg	tgc	ctg	aac	gtg	gag	gtt	ctc	tcc	gca	gac	ggc	act	4097
Gln	Ser	Leu	Cys	Leu	Asn	Val	Glu	Val	Leu	Ser	Ala	Asp	Gly	Thr	
1120							1125					1130			
cca	atg	gag	ctc	gcg	ggt	gac	gac	gac	ttc	gat	cag	gca	ggc		4142
Pro	Met	Glu	Leu	Ala	Gly	Asp	Asp	Asp	Asp	Phe	Asp	Gln	Ala	Gly	
1135							1140					1145			
gcc	tca	ctt	ggc	atc	aac	ctg	tcc	cgt	gac	gag	cgt	tcc	gac	gcc	4187
Ala	Ser	Leu	Gly	Ile	Asn	Leu	Ser	Arg	Asp	Glu	Arg	Ser	Asp	Ala	
1150							1155					1160			
gac	acc	gca	tagcagatca	gaaaacaacc	gctagaaatc	aagccataca									4236
Asp	Thr	Ala													
1165															
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cgtcttcgat	gagctccgca	tcggcctggc	caccggccgac	gacatccgcc	gttggtccaa										4356
gggtgaggtc	aagaagccgg	agaccatcaa	ctaccgaacc	ctcaagcctg	agaaggacgg										4416
tctgttctgc	gagcgtatct	tcggtccaac	tcgcgactgg	gagtgcgcct	gcggtaagta										4476
caagcgtgtc	cgctacaagg	gcatcatctg	tgaacgctgt	ggcgttgagg	tcaccaagtc										4536
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ggacctcatc	atctacttcg	gtgcgaacat	catcaccagc	gtggacgaag	aggctcgcca										4716
cagcgtacc	accactttg	aggcagaaat	gcttctggag	aagaaggacg	ttgaggcaga										4776
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gcagcacatc	cgtgagcgtg	cacagcgcga	aatcgatcgt	ctcgatgagg	tctggcagac										4956
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<210> 4
 <211> 1165
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 4

Val Leu Glu Gly Leu Ile Leu Ala Val Ser Arg Gln Thr Lys Ser Val
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Val Asp Ile Pro Gly Ala Pro Gln Arg Tyr Ser Phe Ala Lys Val Ser
20 25 30

Ala Pro Ile Glu Val Pro Gly Leu Leu Asp Leu Gln Leu Asp Ser Tyr
35 40 45

Ser Trp Leu Ile Gly Thr Pro Glu Trp Arg Ala Arg Gln Lys Glu Glu
50 55 60

Phe Gly Glu Gly Ala Arg Val Thr Ser Gly Leu Glu Asn Ile Leu Glu
65 70 75 80

Glu Leu Ser Pro Ile Gln Asp Tyr Ser Gly Asn Met Ser Leu Ser Leu
85 90 95

Ser Glu Pro Arg Phe Glu Asp Val Lys Asn Thr Ile Asp Glu Ala Lys
100 105 110

Glu Lys Asp Ile Asn Tyr Ala Ala Pro Leu Tyr Val Thr Ala Glu Phe
115 120 125

Val Asn Asn Thr Thr Gly Glu Ile Lys Ser Gln Thr Val Phe Ile Gly
130 135 140

Asp Phe Pro Met Met Thr Asp Lys Gly Thr Phe Ile Ile Asn Gly Thr
145 150 155 160

Glu Arg Val Val Val Ser Gln Leu Val Arg Ser Pro Gly Val Tyr Phe
165 170 175

Asp Gln Thr Ile Asp Lys Ser Thr Glu Arg Pro Leu His Ala Val Lys
180 185 190

Val Ile Pro Phe Arg Gly Ala Trp Leu Glu Phe Asp Val Asp Lys Arg
195 200 205

Asp Ser Val Gly Val Arg Ile Asp Arg Lys Arg Arg Gln Pro Val Thr
210 215 220

Val Leu Leu Lys Ala Leu Gly Trp Thr Thr Glu Gln Ile Thr Glu Arg

225

230

235

240

Phe Gly Phe Ser Glu Ile Met Met Ser Thr Leu Glu Ser Asp Gly Val
245 250 255

Ala Asn Thr Asp Glu Ala Leu Leu Glu Ile Tyr Arg Lys Gln Arg Pro
260 265 270

Gly Glu Gln Pro Thr Arg Asp Leu Ala Gln Ser Leu Leu Asp Asn Ser
275 280 285

Phe Phe Arg Ala Lys Arg Tyr Asp Leu Ala Arg Val Gly Arg Tyr Lys
290 295 300

Ile Asn Arg Lys Leu Gly Leu Gly Gly Asp His Asp Gly Leu Met Thr
305 310 315 320

Leu Thr Glu Glu Asp Ile Ala Thr Thr Ile Glu Tyr Leu Val Arg Leu
325 330 335

His Ala Gly Glu Arg Val Met Thr Ser Pro Asn Gly Glu Glu Ile Pro
340 345 350

Val Glu Thr Asp Asp Ile Asp His Phe Gly Asn Arg Arg Leu Arg Thr
355 360 365

Val Gly Glu Leu Ile Gln Asn Gln Val Arg Val Gly Leu Ser Arg Met
370 375 380

Glu Arg Val Val Arg Glu Arg Met Thr Thr Gln Asp Ala Glu Ser Ile
385 390 395 400

Thr Pro Thr Ser Leu Ile Asn Val Arg Pro Val Ser Ala Ala Ile Arg
405 410 415

Glu Phe Phe Gly Thr Ser Gln Leu Ser Gln Phe Met Val Gln Asn Asn
420 425 430

Ser Leu Ser Gly Leu Thr His Lys Arg Arg Leu Ser Ala Leu Gly Pro
435 440 445

Gly Gly Leu Ser Arg Glu Arg Ala Gly Ile Glu Val Arg Asp Val His
450 455 460

Pro Ser His Tyr Gly Arg Met Cys Pro Ile Glu Thr Pro Glu Gly Pro
465 470 475 480

Asn Ile Gly Leu Ile Gly Ser Leu Ala Ser Tyr Ala Arg Val Asn Pro
485 490 495

Phe Gly Phe Ile Glu Thr Pro Tyr Arg Arg Ile Ile Asp Gly Lys Leu
500 505 510

Thr Asp Gln Ile Asp Tyr Leu Thr Ala Asp Glu Glu Asp Arg Phe Val
515 520 525

Val Ala Gln Ala Asn Thr His Tyr Asp Glu Glu Gly Asn Ile Thr Asp
530 535 540

Glu Thr Val Thr Val Arg Leu Lys Asp Gly Asp Ile Ala Met Val Gly
545 550 555 560

Arg Asn Ala Val Asp Tyr Met Asp Val Ser Pro Arg Gln Met Val Ser
565 570 575

Val Gly Thr Ala Met Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg
580 585 590

Ala Leu Met Gly Ala Asn Met Gln Lys Gln Ala Val Pro Leu Ile Arg
595 600 605

Ala Glu Ala Pro Phe Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr
610 615 620

Asp Ala Gly Asp Leu Val Ile Thr Pro Val Ala Gly Val Val Glu Asn
625 630 635 640

Val Ser Ala Asp Phe Ile Thr Ile Met Ala Asp Asp Gly Lys Arg Glu
645 650 655

Thr Tyr Leu Leu Arg Lys Phe Gln Arg Thr Asn Gln Gly Thr Ser Tyr
660 665 670

Asn Gln Lys Pro Leu Val Asn Leu Gly Glu Arg Val Glu Ala Gly Gln
675 680 685

Val Ile Ala Asp Gly Pro Gly Thr Phe Asn Gly Glu Met Ser Leu Gly
690 695 700

Arg Asn Leu Leu Val Ala Phe Met Pro Trp Glu Gly His Asn Tyr Glu
705 710 715 720

Asp Ala Ile Ile Leu Asn Gln Asn Ile Val Glu Gln Asp Ile Leu Thr
725 730 735

Ser Ile His Ile Glu Glu His Glu Ile Asp Ala Arg Asp Thr Lys Leu
740 745 750

Gly Ala Glu Glu Ile Thr Arg Asp Ile Pro Asn Val Ser Glu Glu Val
755 760 765

Leu Lys Asp Leu Asp Asp Arg Gly Ile Val Arg Ile Gly Ala Asp Val
770 775 780

Arg Asp Gly Asp Ile Leu Val Gly Lys Val Thr Pro Lys Gly Glu Thr
785 790 795 800

Glu Leu Thr Pro Glu Glu Arg Leu Leu Arg Ala Ile Phe Gly Glu Lys
805 810 815

Ala Arg Glu Val Arg Asp Thr Ser Met Lys Val Pro His Gly Glu Thr
820 825 830

Gly Lys Val Ile Gly Val Arg His Phe Ser Arg Glu Asp Asp Asp Asp
835 840 845

Leu Ala Pro Gly Val Asn Glu Met Ile Arg Ile Tyr Val Ala Gln Lys
850 855 860

Arg Lys Ile Gln Asp Gly Asp Lys Leu Ala Gly Arg His Gly Asn Lys
865 870 875 880

Gly Val Val Gly Lys Ile Leu Pro Gln Glu Asp Met Pro Phe Leu Pro
885 890 895

Asp Gly Thr Pro Val Asp Ile Ile Leu Asn Thr His Gly Val Pro Arg
900 905 910

Arg Met Asn Ile Gly Gln Val Leu Glu Thr His Leu Gly Trp Leu Ala
915 920 925

Ser Ala Gly Trp Ser Val Asp Pro Glu Asp Pro Glu Asn Ala Glu Leu
930 935 940

Val Lys Thr Leu Pro Ala Asp Leu Leu Glu Val Pro Ala Gly Ser Leu
945 950 955 960

Thr Ala Thr Pro Val Phe Asp Gly Ala Ser Asn Glu Glu Leu Ala Gly
965 970 975

Leu Leu Ala Asn Ser Arg Pro Asn Arg Asp Gly Asp Val Met Val Asn
980 985 990

Ala Asp Gly Lys Ala Thr Leu Ile Asp Gly Arg Ser Gly Glu Pro Tyr
995 1000 1005

Pro Tyr Pro Val Ser Ile Gly Tyr Met Tyr Met Leu Lys Leu His
1010 1015 1020

His Leu Val Asp Glu Lys Ile His Ala Arg Ser Thr Gly Pro Tyr
1025 1030 1035

Ser Met Ile Thr Gln Gln Pro Leu Gly Gly Lys Ala Gln Phe Gly
1040 1045 1050

Gly Gln Arg Phe Gly Glu Met Glu Val Trp Ala Met Gln Ala Tyr
1055 1060 1065

Gly Ala Ala Tyr Thr Leu Gln Glu Leu Leu Thr Ile Lys Ser Asp
1070 1075 1080

Asp Val Val Gly Arg Val Lys Val Tyr Glu Ala Ile Val Lys Gly
1085 1090 1095

Glu Asn Ile Pro Asp Pro Gly Ile Pro Glu Ser Phe Lys Val Leu
1100 1105 1110

Leu Lys Glu Leu Gln Ser Leu Cys Leu Asn Val Glu Val Leu Ser
1115 1120 1125

Ala Asp Gly Thr Pro Met Glu Leu Ala Gly Asp Asp Asp Asp Phe

1130

1135

1140

Asp Gln Ala Gly Ala Ser Leu Gly Ile Asn Leu Ser Arg Asp Glu
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Arg Ser Asp Ala Asp Thr Ala
1160 1165

<210> 5
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<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (702)..(4196)
<223>

<220>
<221> mutation
<222> (2016)..(2016)
<223> Substitution of cytosine by thymine

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tcgacgcctc cctcgacgat gcagctgtct ctaagctggc tgcacaggcc gaaagcatcc 120
ctgatggaga tgtgagcaaa atcgcääata ccgtaggtat tgtgatcggt gcggatttgg
ctctcggtgg cctggccggg tttttgggg cgtttggaa gaaacgtcga gaagcttaac 180
ctgctgttca aatagatttt ccctgtttcg aattgcggaa accccgggtt ttttgctag
ggtgccctcgta agaagggttc aagaagattt ctgggaaacg cggccgtcgc gttgggtgct 240
aatagcacgc ggagcaccag atgaaaaatc tcccctttac tttcgccgc gattggata 300
ctctgagtcg ttgcgttgaa attcgtgact cttttcggtt cctgtagcgc caagaccctt 360
atcaaggtgg tttaaaaaaa ccgatttgac aaggtcattc agtgcatact ggagtctttc
agggggatcg gttccctcag cagaccaatt gctaaaaat accagcggtg ttgatctgca 420
cttaatggcc ttgaccagcc aggtgcaatt acccgctgtga g gtg ctg gaa gga ccc 480
Val Leu Glu Gly Pro
1 5
716

atc ttg gca gtc tcc cgc cag acc aag tca gtc gtc gat att ccc ggt 764
Ile Leu Ala Val Ser Arg Gln Thr Lys Ser Val Val Asp Ile Pro Gly

10	15	20	
gca ccg cag cgt tat tct ttc gcg aag gtg tcc gca ccc att gag gtg Ala Pro Gln Arg Tyr Ser Phe Ala Lys Val Ser Ala Pro Ile Glu Val 25	30	35	812
ccc ggg cta cta gat ctt caa ctg gat tct tac tcc tgg ctg att ggt Pro Gly Leu Leu Asp Leu Gln Leu Asp Ser Tyr Ser Trp Leu Ile Gly 40	45	50	860
acg cct gag tgg cgt gct cgt cag aag gaa gaa ttc ggc gag gga gcc Thr Pro Glu Trp Arg Ala Arg Gln Lys Glu Glu Phe Gly Glu Gly Ala 55	60	65	908
cgc gta acc agc ggc ctt gag aac att ctc gag gag ctc tcc cca atc Arg Val Thr Ser Gly Leu Glu Asn Ile Leu Glu Glu Leu Ser Pro Ile 70	75	80	956
cag gat tac tct gga aac atg tcc ctg agc ctt tcg gag cca cgc ttc Gln Asp Tyr Ser Gly Asn Met Ser Leu Ser Leu Ser Glu Pro Arg Phe 90	95	100	1004
gaa gac gtc aag aac acc att gac gag gcg aaa gaa aag gac atc aac Glu Asp Val Lys Asn Thr Ile Asp Glu Ala Lys Glu Lys Asp Ile Asn 105	110	115	1052
tac gcg gcg cca ctg tat gtg acc gcg gag ttc gtc aac aac acc acc Tyr Ala Ala Pro Leu Tyr Val Thr Ala Glu Phe Val Asn Asn Thr Thr 120	125	130	1100
ggt gaa atc aag tct cag act gtc ttc atc ggc gat ttc cca atg atg Gly Glu Ile Lys Ser Gln Thr Val Phe Ile Gly Asp Phe Pro Met Met 135	140	145	1148
acg gac aag gga acg ttc atc atc aac gga acc gaa cgc gtt gtg gtc Thr Asp Lys Gly Thr Phe Ile Ile Asn Gly Thr Glu Arg Val Val Val 150	155	160	1196
agc cag ctc gtc cgc tcc ccg ggc gtg tac ttt gac cag acc atc gat Ser Gln Leu Val Arg Ser Pro Gly Val Tyr Phe Asp Gln Thr Ile Asp 170	175	180	1244
aag tca act gag cgt cca ctg cac gcc gtg aag gtt att cct tcc cgt Lys Ser Thr Glu Arg Pro Leu His Ala Val Lys Val Ile Pro Ser Arg 185	190	195	1292
ggt gct tgg ctt gag ttt gac gtc gat aag cgc gat tcg gtt ggt gtt Gly Ala Trp Leu Glu Phe Asp Val Asp Lys Arg Asp Ser Val Gly Val 200	205	210	1340
cgt att gac cgc aag cgt cgc cag cca gtc acc gta ctg ctg aag gct Arg Ile Asp Arg Lys Arg Arg Gln Pro Val Thr Val Leu Leu Lys Ala 215	220	225	1388
ctt ggc tgg acc act gag cag atc acc gag cgt ttc ggt ttc tct gaa Leu Gly Trp Thr Thr Glu Gln Ile Thr Glu Arg Phe Gly Phe Ser Glu 230	235	240	1436
			245

atc atg atg tcc acc ctc gag tcc gat ggt gta gca aac acc gat gag Ile Met Met Ser Thr Leu Glu Ser Asp Gly Val Ala Asn Thr Asp Glu 250 255 260	1484
gca ttg ctg gag atc tac cgc aag cag cgt cca ggc gag cag cct acc Ala Leu Leu Glu Ile Tyr Arg Lys Gln Arg Pro Gly Glu Gln Pro Thr 265 270 275	1532
cgc gac ctt gcg cag tcc ctc ctg gac aac agc ttc ttc cgt gca aag Arg Asp Leu Ala Gln Ser Leu Leu Asp Asn Ser Phe Phe Arg Ala Lys 280 285 290	1580
cgc tac gac ctg gct cgc gtt ggt cgt tac aag atc aac cgc aag ctc Arg Tyr Asp Leu Ala Arg Val Gly Arg Tyr Lys Ile Asn Arg Lys Leu 295 300 305	1628
ggc ctt ggt ggc gac cac gat ggt/ttg atg act ctt act gaa gag gac Gly Leu Gly Asp His Asp Gly Leu Met Thr Leu Thr Glu Glu Asp 310 315 320 325	1676
atc gca acc acc atc gag tac ctg gtg cgt ctg cac gca ggt gag cgc Ile Ala Thr Thr Ile Glu Tyr Leu Val Arg Leu His Ala Gly Glu Arg 330 335 340	1724
gtc atg act tct cca aat ggt gaa gag atc cca gtc gag acc gat gac Val Met Thr Ser Pro Asn Gly Glu Ile Pro Val Glu Thr Asp Asp 345 350 355	1772
atc gac cac ttt ggt aac cgt cgt ctg cgt acc gtt ggc gaa ctg atc Ile Asp His Phe Gly Asn Arg Arg Leu Arg Thr Val Gly Glu Leu Ile 360 365 370	1820
cag aac cag gtc cgt gtc ggc ctg tcc cgc atg gag cgc gtt gtt cgt Gln Asn Gln Val Arg Val Gly Leu Ser Arg Met Glu Arg Val Val Arg 375 380 385	1868
gag cgt atg acc acc cag gat gcg gag tcc att act cct act tcc ttg Glu Arg Met Thr Thr Gln Asp Ala Glu Ser Ile Thr Pro Thr Ser Leu 390 395 400 405	1916
atc aac gtt cgt cct gtc tct gca gct atc cgt gag ttc ttc gga act Ile Asn Val Arg Pro Val Ser Ala Ala Ile Arg Glu Phe Phe Gly Thr 410 415 420	1964
tcc cag ctg tct cag ttc atg gac cag aac aac tcc ctg tct ggt ttg Ser Gln Leu Ser Gln Phe Met Asp Gln Asn Asn Ser Leu Ser Gly Leu 425 430 435	2012
act tac aag cgt cgt ctg gct ctg ggc ccg ggt ctg tcc cgt Thr Tyr Lys Arg Arg Leu Ser Ala Leu Gly Pro Gly Gly Leu Ser Arg 440 445 450	2060
gag cgc gcc ggc atc gag gtt cga gac gtt cac cca tct cac tac ggc Glu Arg Ala Gly Ile Glu Val Arg Asp Val His Pro Ser His Tyr Gly 455 460 465	2108

cgt atg tgc cca att gag act ccg gaa ggt cca aac att ggc ctg atc Arg Met Cys Pro Ile Glu Thr Pro Glu Gly Pro Asn Ile Gly Leu Ile 470 475 480 485	2156
ggt tcc ttg gct tcc tat gct cga gtg aac cca ttc ggt ttc att gag Gly Ser Leu Ala Ser Tyr Ala Arg Val Asn Pro Phe Gly Phe Ile Glu 490 495 500	2204
acc cca tac cgt cgc atc atc gac ggc aag ctg acc gac cag att gac Thr Pro Tyr Arg Arg Ile Ile Asp Gly Lys Leu Thr Asp Gln Ile Asp 505 510 515	2252
tac ctt acc gct gat gag gaa gac cgc ttc gtt gtc cag gca aac Tyr Leu Thr Ala Asp Glu Glu Asp Arg Phe Val Val Ala Gln Ala Asn 520 525 530	2300
acg cac tac gac gaa gag ggc aac atc acc gat gag acc gtc act gtt Thr His Tyr Asp Glu Glu Gly Asn Ile Thr Asp Glu Thr Val Thr Val 535 540 545	2348
cgt ctg aag gac ggc gac atc gcc atg gtt ggc cgc aac gcg gtt gat Arg Leu Lys Asp Gly Asp Ile Ala Met Val Gly Arg Asn Ala Val Asp 550 555 560 565	2396
tac atg gac gtt tcc cct cgt cag atg gtt tct gtt ggt acc gcg atg Tyr Met Asp Val Ser Pro Arg Gln Met Val Ser Val Gly Thr Ala Met 570 575 580	2444
att cca ttc ctg gag cac gac gat gct aac cgt gca ctg atg ggc gcg Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg Ala Leu Met Gly Ala 585 590 595	2492
aac atg cag aag cag gct gtg cca ctg att cgt gcc gag gct cct ttc Asn Met Gln Lys Gln Ala Val Pro Leu Ile Arg Ala Glu Ala Pro Phe 600 605 610	2540
gtg ggc acc ggt atg gag cag cgc gca gca tac gac gcc ggc gac ctg Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr Asp Ala Gly Asp Leu 615 620 625	2588
gtt att acc cca gtc gca ggt gtg gtg gaa aac gtt tca gct gac ttc Val Ile Thr Pro Val Ala Gly Val Val Glu Asn Val Ser Ala Asp Phe 630 635 640 645	2636
atc acc atc atg gct gat gac ggc aag cgc gaa acc tac ctg ctg cgt Ile Thr Ile Met Ala Asp Asp Gly Lys Arg Glu Thr Tyr Leu Leu Arg 650 655 660	2684
aag ttc cag cgc acc aac cag ggc acc agc tac aac cag aag cct ttg Lys Phe Gln Arg Thr Asn Gln Gly Thr Ser Tyr Asn Gln Lys Pro Leu 665 670 675	2732
gtt aac ttg ggc gag cgc gtt gaa gct ggc cag gtt att gct gat ggt Val Asn Leu Gly Glu Arg Val Glu Ala Gly Gln Val Ile Ala Asp Gly 680 685 690	2780
cca ggt acc ttc aat ggt gaa atg tcc ctt ggc cgt aac ctt ctg gtt	2828

Pro	Gly	Thr	Phe	Asn	Gly	Glu	Met	Ser	Leu	Gly	Arg	Asn	Leu	Leu	Val	
695																
gct	tcc	atg	cct	tgg	gaa	ggc	cac	aac	tac	gag	gat	gct	atc	atc	ctc	2876
Ala	Phe	Met	Pro	Trp	Glu	Gly	His	Asn	Tyr	Glu	Asp	Ala	Ile	Ile	Leu	
710					715					720					725	
aac	cag	aac	atc	gtt	gag	cag	gac	atc	ttg	acc	tcg	atc	cac	atc	gag	2924
Asn	Gln	Asn	Ile	Val	Glu	Gln	Asp	Ile	Leu	Thr	Ser	Ile	His	Ile	Glu	
					730				735						740	
gag	cac	gag	atc	gat	gcc	cgc	gac	act	aag	ctt	ggc	gcc	gaa	atc		2972
Glu	His	Glu	Ile	Asp	Ala	Arg	Asp	Thr	Lys	Leu	Gly	Ala	Glu	Glu	Ile	
					745				750						755	
acc	cgc	gac	atc	cct	aat	gtg	tct	gaa	gaa	gtc	ctc	aag	gac	ctc	gac	3020
Thr	Arg	Asp	Ile	Pro	Asn	Val	Ser	Glu	Glu	Val	Leu	Lys	Asp	Leu	Asp	
					760			765			770					
gac	cgc	ggt	att	gtc	cgc	atc	ggt	gct	gat	gtt	cgt	gac	ggc	gac	atc	3068
Asp	Arg	Gly	Ile	Val	Arg	Ile	Gly	Ala	Asp	Val	Arg	Asp	Gly	Asp	Ile	
					775			780			785					
ctg	gtc	ggt	aag	gtc	acc	cct	aag	ggc	gag	acc	gag	ctc	acc	ccg	gaa	3116
Leu	Val	Gly	Lys	Val	Thr	Pro	Lys	Gly	Glu	Thr	Glu	Leu	Thr	Pro	Glu	
					790			795			800				805	
gag	cgc	ttg	ctg	cgc	gca	atc	ttc	ggt	gag	aag	gcc	cgc	gaa	gtt	cgc	3164
Glu	Arg	Leu	Leu	Arg	Ala	Ile	Phe	Gly	Glu	Lys	Ala	Arg	Glu	Val	Arg	
					810			815			820					
gat	acc	tcc	atg	aag	gtg	cct	cac	ggt	gag	acc	ggc	aag	gtc	atc	ggc	3212
Asp	Thr	Ser	Met	Lys	Val	Pro	His	Gly	Glu	Thr	Gly	Lys	Val	Ile	Gly	
					825			830			835					
gtg	cgt	cac	tcc	tcc	cgc	gag	gac	gac	gat	ctg	gct	cct	ggc	gtc		3260
Val	Arg	His	Phe	Ser	Arg	Glu	Asp	Asp	Asp	Asp	Leu	Ala	Pro	Gly	Val	
					840			845			850					
aac	gag	atg	atc	cgt	atc	tac	gtt	gct	cag	aag	cgt	aag	atc	cag	gac	3308
Asn	Glu	Met	Ile	Arg	Ile	Tyr	Val	Ala	Gln	Lys	Arg	Lys	Ile	Gln	Asp	
					855			860			865					
ggc	gat	aag	ctc	gct	ggc	cgc	cac	ggt	aac	aag	ggt	gtt	gtc	ggt	aaa	3356
Gly	Asp	Lys	Leu	Ala	Gly	Arg	His	Gly	Asn	Lys	Gly	Val	Val	Gly	Lys	
					870			875			880				885	
att	ttg	cct	cag	gaa	gat	atg	cca	ttc	ctt	cca	gac	ggc	act	cct	gtt	3404
Ile	Leu	Pro	Gln	Glu	Asp	Met	Pro	Phe	Leu	Pro	Asp	Gly	Thr	Pro	Val	
					890			895			900					
gac	atc	atc	ttg	aac	acc	cac	ggt	gtt	cca	cgt	cgt	atg	aac	att	ggt	3452
Asp	Ile	Ile	Leu	Asn	Thr	His	Gly	Val	Pro	Arg	Arg	Met	Asn	Ile	Gly	
					905			910			915					
cag	gtt	ctt	gag	acc	cac	ttt	ggc	tgg	ctg	gca	tct	gct	ggt	tgg	tcc	3500
Gln	Val	Leu	Glu	Thr	His	Leu	Gly	Trp	Leu	Ala	Ser	Ala	Gly	Trp	Ser	

DNA sequence (5' to 3' direction)

920

925

930

gtg gat cct gaa gat cct gag aac gct gag ctc gtc aag act ctg cct	3548																																																																																																										
Val Asp Pro Glu Asp Pro Glu Asn Ala Glu Leu Val Lys Thr Leu Pro																																																																																																											
935	940	945		gca gac ctc ctc gag gtt cct gct ggt tcc ttg act gca act cct gtg	3596	Ala Asp Leu Leu Glu Val Pro Ala Gly Ser Leu Thr Ala Thr Pro Val		950	955	960	965	ttc gac ggt gcg tca aac gaa gag ctc gca ggc ctg ctc gct aat tca	3644	Phe Asp Gly Ala Ser Asn Glu Glu Leu Ala Gly Leu Leu Ala Asn Ser		970	975	980		cgt cca aac cgc gac ggc gac gtc atg gtt aac gcg gat ggt aaa gca	3692	Arg Pro Asn Arg Asp Gly Asp Val Met Val Asn Ala Asp Gly Lys Ala		985	990	995		acg ctt atc gac ggt cgc tcc ggt gag cct tac ccg tac ccg gtt	3737	Thr Leu Ile Asp Gly Arg Ser Gly Glu Pro Tyr Pro Tyr Pro Val		1000	1005	1010		tcc atc ggc tac atg tac atg ctg aag ctg cac cac ctc gtt gac	3782	Ser Ile Gly Tyr Met Tyr Met Leu Lys Leu His His Leu Val Asp		1015	1020	1025		gag aag atc cac gca cgt tcc act ggt cct tac tcc atg att acc	3827	Glu Lys Ile His Ala Arg Ser Thr Gly Pro Tyr Ser Met Ile Thr		1030	1035	1040		cag cag cca ctg ggt ggt aaa gca cag ttc ggt gga cag cgt ttc	3872	Gln Gln Pro Leu Gly Gly Lys Ala Gln Phe Gly Gly Gln Arg Phe		1045	1050	1055		ggc gaa atg gag gtg tgg gca atg cag gca tac ggc gct gcc tac	3917	Gly Glu Met Glu Val Trp Ala Met Gln Ala Tyr Gly Ala Ala Tyr		1060	1065	1070		aca ctt cag gag ctg ctg acc atc aag tct gat gac gtg gtt ggc	3962	Thr Leu Gln Glu Leu Leu Thr Ile Lys Ser Asp Asp Val Val Gly		1075	1080	1085		cgt gtc aag gtc tac gaa gca att gtg aag ggc gag aac atc ccg	4007	Arg Val Lys Val Tyr Glu Ala Ile Val Lys Gly Glu Asn Ile Pro		1090	1095	1100		gat cca ggt att cct gag tcc ttc aag gtt ctc ctc aag gag ctc	4052	Asp Pro Gly Ile Pro Glu Ser Phe Lys Val Leu Leu Lys Glu Leu		1105	1110	1115		cag tcc ttg tgc ctg aac gtg gag gtt ctc tcc gca gac ggc act	4097	Gln Ser Leu Cys Leu Asn Val Glu Val Leu Ser Ala Asp Gly Thr		1120	1125	1130		cca atg gag ctc gcg ggt gac gac gac gac ttc gat cag gca ggc	4142	Pro Met Glu Leu Ala Gly Asp Asp Asp Asp Phe Asp Gln Ala Gly		1135	1140	1145	
945																																																																																																											
gca gac ctc ctc gag gtt cct gct ggt tcc ttg act gca act cct gtg	3596																																																																																																										
Ala Asp Leu Leu Glu Val Pro Ala Gly Ser Leu Thr Ala Thr Pro Val																																																																																																											
950	955	960	965	ttc gac ggt gcg tca aac gaa gag ctc gca ggc ctg ctc gct aat tca	3644	Phe Asp Gly Ala Ser Asn Glu Glu Leu Ala Gly Leu Leu Ala Asn Ser		970	975	980		cgt cca aac cgc gac ggc gac gtc atg gtt aac gcg gat ggt aaa gca	3692	Arg Pro Asn Arg Asp Gly Asp Val Met Val Asn Ala Asp Gly Lys Ala		985	990	995		acg ctt atc gac ggt cgc tcc ggt gag cct tac ccg tac ccg gtt	3737	Thr Leu Ile Asp Gly Arg Ser Gly Glu Pro Tyr Pro Tyr Pro Val		1000	1005	1010		tcc atc ggc tac atg tac atg ctg aag ctg cac cac ctc gtt gac	3782	Ser Ile Gly Tyr Met Tyr Met Leu Lys Leu His His Leu Val Asp		1015	1020	1025		gag aag atc cac gca cgt tcc act ggt cct tac tcc atg att acc	3827	Glu Lys Ile His Ala Arg Ser Thr Gly Pro Tyr Ser Met Ile Thr		1030	1035	1040		cag cag cca ctg ggt ggt aaa gca cag ttc ggt gga cag cgt ttc	3872	Gln Gln Pro Leu Gly Gly Lys Ala Gln Phe Gly Gly Gln Arg Phe		1045	1050	1055		ggc gaa atg gag gtg tgg gca atg cag gca tac ggc gct gcc tac	3917	Gly Glu Met Glu Val Trp Ala Met Gln Ala Tyr Gly Ala Ala Tyr		1060	1065	1070		aca ctt cag gag ctg ctg acc atc aag tct gat gac gtg gtt ggc	3962	Thr Leu Gln Glu Leu Leu Thr Ile Lys Ser Asp Asp Val Val Gly		1075	1080	1085		cgt gtc aag gtc tac gaa gca att gtg aag ggc gag aac atc ccg	4007	Arg Val Lys Val Tyr Glu Ala Ile Val Lys Gly Glu Asn Ile Pro		1090	1095	1100		gat cca ggt att cct gag tcc ttc aag gtt ctc ctc aag gag ctc	4052	Asp Pro Gly Ile Pro Glu Ser Phe Lys Val Leu Leu Lys Glu Leu		1105	1110	1115		cag tcc ttg tgc ctg aac gtg gag gtt ctc tcc gca gac ggc act	4097	Gln Ser Leu Cys Leu Asn Val Glu Val Leu Ser Ala Asp Gly Thr		1120	1125	1130		cca atg gag ctc gcg ggt gac gac gac gac ttc gat cag gca ggc	4142	Pro Met Glu Leu Ala Gly Asp Asp Asp Asp Phe Asp Gln Ala Gly		1135	1140	1145									
960	965																																																																																																										
ttc gac ggt gcg tca aac gaa gag ctc gca ggc ctg ctc gct aat tca	3644																																																																																																										
Phe Asp Gly Ala Ser Asn Glu Glu Leu Ala Gly Leu Leu Ala Asn Ser																																																																																																											
970	975	980		cgt cca aac cgc gac ggc gac gtc atg gtt aac gcg gat ggt aaa gca	3692	Arg Pro Asn Arg Asp Gly Asp Val Met Val Asn Ala Asp Gly Lys Ala		985	990	995		acg ctt atc gac ggt cgc tcc ggt gag cct tac ccg tac ccg gtt	3737	Thr Leu Ile Asp Gly Arg Ser Gly Glu Pro Tyr Pro Tyr Pro Val		1000	1005	1010		tcc atc ggc tac atg tac atg ctg aag ctg cac cac ctc gtt gac	3782	Ser Ile Gly Tyr Met Tyr Met Leu Lys Leu His His Leu Val Asp		1015	1020	1025		gag aag atc cac gca cgt tcc act ggt cct tac tcc atg att acc	3827	Glu Lys Ile His Ala Arg Ser Thr Gly Pro Tyr Ser Met Ile Thr		1030	1035	1040		cag cag cca ctg ggt ggt aaa gca cag ttc ggt gga cag cgt ttc	3872	Gln Gln Pro Leu Gly Gly Lys Ala Gln Phe Gly Gly Gln Arg Phe		1045	1050	1055		ggc gaa atg gag gtg tgg gca atg cag gca tac ggc gct gcc tac	3917	Gly Glu Met Glu Val Trp Ala Met Gln Ala Tyr Gly Ala Ala Tyr		1060	1065	1070		aca ctt cag gag ctg ctg acc atc aag tct gat gac gtg gtt ggc	3962	Thr Leu Gln Glu Leu Leu Thr Ile Lys Ser Asp Asp Val Val Gly		1075	1080	1085		cgt gtc aag gtc tac gaa gca att gtg aag ggc gag aac atc ccg	4007	Arg Val Lys Val Tyr Glu Ala Ile Val Lys Gly Glu Asn Ile Pro		1090	1095	1100		gat cca ggt att cct gag tcc ttc aag gtt ctc ctc aag gag ctc	4052	Asp Pro Gly Ile Pro Glu Ser Phe Lys Val Leu Leu Lys Glu Leu		1105	1110	1115		cag tcc ttg tgc ctg aac gtg gag gtt ctc tcc gca gac ggc act	4097	Gln Ser Leu Cys Leu Asn Val Glu Val Leu Ser Ala Asp Gly Thr		1120	1125	1130		cca atg gag ctc gcg ggt gac gac gac gac ttc gat cag gca ggc	4142	Pro Met Glu Leu Ala Gly Asp Asp Asp Asp Phe Asp Gln Ala Gly		1135	1140	1145																	
980																																																																																																											
cgt cca aac cgc gac ggc gac gtc atg gtt aac gcg gat ggt aaa gca	3692																																																																																																										
Arg Pro Asn Arg Asp Gly Asp Val Met Val Asn Ala Asp Gly Lys Ala																																																																																																											
985	990	995		acg ctt atc gac ggt cgc tcc ggt gag cct tac ccg tac ccg gtt	3737	Thr Leu Ile Asp Gly Arg Ser Gly Glu Pro Tyr Pro Tyr Pro Val		1000	1005	1010		tcc atc ggc tac atg tac atg ctg aag ctg cac cac ctc gtt gac	3782	Ser Ile Gly Tyr Met Tyr Met Leu Lys Leu His His Leu Val Asp		1015	1020	1025		gag aag atc cac gca cgt tcc act ggt cct tac tcc atg att acc	3827	Glu Lys Ile His Ala Arg Ser Thr Gly Pro Tyr Ser Met Ile Thr		1030	1035	1040		cag cag cca ctg ggt ggt aaa gca cag ttc ggt gga cag cgt ttc	3872	Gln Gln Pro Leu Gly Gly Lys Ala Gln Phe Gly Gly Gln Arg Phe		1045	1050	1055		ggc gaa atg gag gtg tgg gca atg cag gca tac ggc gct gcc tac	3917	Gly Glu Met Glu Val Trp Ala Met Gln Ala Tyr Gly Ala Ala Tyr		1060	1065	1070		aca ctt cag gag ctg ctg acc atc aag tct gat gac gtg gtt ggc	3962	Thr Leu Gln Glu Leu Leu Thr Ile Lys Ser Asp Asp Val Val Gly		1075	1080	1085		cgt gtc aag gtc tac gaa gca att gtg aag ggc gag aac atc ccg	4007	Arg Val Lys Val Tyr Glu Ala Ile Val Lys Gly Glu Asn Ile Pro		1090	1095	1100		gat cca ggt att cct gag tcc ttc aag gtt ctc ctc aag gag ctc	4052	Asp Pro Gly Ile Pro Glu Ser Phe Lys Val Leu Leu Lys Glu Leu		1105	1110	1115		cag tcc ttg tgc ctg aac gtg gag gtt ctc tcc gca gac ggc act	4097	Gln Ser Leu Cys Leu Asn Val Glu Val Leu Ser Ala Asp Gly Thr		1120	1125	1130		cca atg gag ctc gcg ggt gac gac gac gac ttc gat cag gca ggc	4142	Pro Met Glu Leu Ala Gly Asp Asp Asp Asp Phe Asp Gln Ala Gly		1135	1140	1145																									
995																																																																																																											
acg ctt atc gac ggt cgc tcc ggt gag cct tac ccg tac ccg gtt	3737																																																																																																										
Thr Leu Ile Asp Gly Arg Ser Gly Glu Pro Tyr Pro Tyr Pro Val																																																																																																											
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1010																																																																																																											
tcc atc ggc tac atg tac atg ctg aag ctg cac cac ctc gtt gac	3782																																																																																																										
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Glu Lys Ile His Ala Arg Ser Thr Gly Pro Tyr Ser Met Ile Thr																																																																																																											
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Phe Gly Glu Gly Ala Arg Val Thr Ser Gly Leu Glu Asn Ile Leu Glu
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Ser Glu Pro Arg Phe Glu Asp Val Lys Asn Thr Ile Asp Glu Ala Lys
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Glu Lys Asp Ile Asn Tyr Ala Ala Pro Leu Tyr Val Thr Ala Glu Phe
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Gly Glu Gln Pro Thr Arg Asp Leu Ala Gln Ser Leu Leu Asp Asn Ser
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Phe Phe Arg Ala Lys Arg Tyr Asp Leu Ala Arg Val Gly Arg Tyr Lys
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Ile Asn Arg Lys Leu Gly Leu Gly Asp His Asp Gly Leu Met Thr
305 310 315 320

Leu Thr Glu Glu Asp Ile Ala Thr Thr Ile Glu Tyr Leu Val Arg Leu
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His Ala Gly Glu Arg Val Met Thr Ser Pro Asn Gly Glu Glu Ile Pro
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Val Glu Thr Asp Asp Ile Asp His Phe Gly Asn Arg Arg Leu Arg Thr
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Val Gly Glu Leu Ile Gln Asn Gln Val Arg Val Gly Leu Ser Arg Met
370 375 380

Glu Arg Val Val Arg Glu Arg Met Thr Thr Gln Asp Ala Glu Ser Ile
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Thr Pro Thr Ser Leu Ile Asn Val Arg Pro Val Ser Ala Ala Ile Arg
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Asn Ile Gly Leu Ile Gly Ser Leu Ala Ser Tyr Ala Arg Val Asn Pro
485 490 495

Phe Gly Phe Ile Glu Thr Pro Tyr Arg Arg Ile Ile Asp Gly Lys Leu
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515 520 525

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Glu Thr Val Thr Val Arg Leu Lys Asp Gly Asp Ile Ala Met Val Gly
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Arg Asn Ala Val Asp Tyr Met Asp Val Ser Pro Arg Gln Met Val Ser
565 570 575

Val Gly Thr Ala Met Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg
580 585 590

Ala Leu Met Gly Ala Asn Met Gln Lys Gln Ala Val Pro Leu Ile Arg
595 600 605

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Asp Ala Gly Asp Leu Val Ile Thr Pro Val Ala Gly Val Val Glu Asn
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Val Ser Ala Asp Phe Ile Thr Ile Met Ala Asp Asp Gly Lys Arg Glu
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675 680 685

Val Ile Ala Asp Gly Pro Gly Thr Phe Asn Gly Glu Met Ser Leu Gly
690 695 700

Arg Asn Leu Leu Val Ala Phe Met Pro Trp Glu Gly His Asn Tyr Glu
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Asp Ala Ile Ile Leu Asn Gln Asn Ile Val Glu Gln Asp Ile Leu Thr

725

730

735

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770 775 780

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785 790 795 800

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Ala Arg Glu Val Arg Asp Thr Ser Met Lys Val Pro His Gly Glu Thr
820 825 830

Gly Lys Val Ile Gly Val Arg His Phe Ser Arg Glu Asp Asp Asp Asp
835 840 845

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850 855 860

Arg Lys Ile Gln Asp Gly Asp Lys Leu Ala Gly Arg His Gly Asn Lys
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Gly Val Val Gly Lys Ile Leu Pro Gln Glu Asp Met Pro Phe Leu Pro
885 890 895

Asp Gly Thr Pro Val Asp Ile Ile Leu Asn Thr His Gly Val Pro Arg
900 905 910

Arg Met Asn Ile Gly Gln Val Leu Glu Thr His Leu Gly Trp Leu Ala
915 920 925

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930 935 940

Val Lys Thr Leu Pro Ala Asp Leu Leu Glu Val Pro Ala Gly Ser Leu
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Leu Leu Ala Asn Ser Arg Pro Asn Arg Asp Gly Asp Val Met Val Asn
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Ala Asp Gly Lys Ala Thr Leu Ile Asp Gly Arg Ser Gly Glu Pro Tyr
995 1000 1005

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Pro Gln Arg Arg Gly Val Cys Thr Arg Val Tyr Thr Thr Pro Lys
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Lys Pro Asn Ser Ala Leu Arg Lys Val Ala Arg Val Arg Leu Thr Ser
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Val Cys Thr Arg Val Tyr Thr Thr Pro Lys Lys Pro Asn Ser Ala		
35	40	45

Leu Arg Lys Val Ala Arg Val Arg Leu Thr Ser Gly Ile Glu Val Ser
50 55 60

Ala Tyr Ile Pro Gly Glu Gly His Asn Leu Gln Glu His Ser Met Val
65 70 75 80

Leu Val Arg Gly Gly Arg Val Lys Asp Leu Pro Gly Val Arg Tyr Lys
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Ile Val Arg Gly Ala Leu Asp Thr Gln Gly Val Lys Asp Arg Lys Gln
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